

	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5	2.6	2.7	2.8	2.9	3.0	3.1	3.2	3.3	3.4	3.5	3.6	3.7	3.8	3.9	4.0	4.1	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	5.0	5.1	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	6.0	6.1	6.2	6.3	6.4	6.5	6.6	6.7	6.8	6.9	7.0	7.1	7.2	7.3	7.4	7.5	7.6	7.7	7.8	7.9	8.0	8.1	8.2	8.3	8.4	8.5	8.6	8.7	8.8	8.9	9.0	9.1	9.2	9.3	9.4	9.5	9.6	9.7	9.8	9.9
0.0	0.0000	0.0001	0.0002	0.0003	0.0004	0.0005	0.0006	0.0007	0.0008	0.0009	0.0010	0.0011	0.0012	0.0013	0.0014	0.0015	0.0016	0.0017	0.0018	0.0019	0.0020	0.0021	0.0022	0.0023	0.0024	0.0025	0.0026	0.0027	0.0028	0.0029	0.0030	0.0031	0.0032	0.0033	0.0034	0.0035	0.0036	0.0037	0.0038	0.0039	0.0040	0.0041	0.0042	0.0043	0.0044	0.0045	0.0046	0.0047	0.0048	0.0049	0.0050	0.0051	0.0052	0.0053	0.0054	0.0055	0.0056	0.0057	0.0058	0.0059	0.0060	0.0061	0.0062	0.0063	0.0064	0.0065	0.0066	0.0067	0.0068	0.0069	0.0070	0.0071	0.0072	0.0073	0.0074	0.0075	0.0076	0.0077	0.0078	0.0079	0.0080	0.0081	0.0082	0.0083	0.0084	0.0085	0.0086	0.0087	0.0088	0.0089	0.0090	0.0091	0.0092	0.0093	0.0094	0.0095	0.0096	0.0097	0.0098	0.0099

The present invention relates to compositions, apparatus and methods useful for concurrently performing multiple, high throughput, biological or chemical assays, using repeated arrays of probes. A combination of the invention comprises a surface, which comprises a plurality of test regions, at least two of which, and in a preferred embodiment, at least twenty of which, are substantially identical, wherein each of the test regions comprises an array of generic anchor molecules. The anchors are associated with bifunctional linker molecules, each containing a portion which is specific for at least one of the anchors and a portion which is a probe specific for a target of interest. The resulting array of probes is used to analyze the presence or test the activity of one or more target molecules which specifically interact with the probes. In one embodiment of the invention, the test regions (which can be wells) are further subdivided into smaller subregions (indentations, or dimples). In one embodiment of the invention, ESTs are mapped. In another embodiment, the presence of a target nucleic acid is detected by protecting the target against nuclease digestion with a polynucleotide fragment, and analyzing the protected polynucleotide by mass spectrometry.